



0590
JLS

RAW SEQUENCE LISTING ERROR REPORT

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Application Serial Number: 09/982,835
Source: OIPE
Date Processed by STIC: 6-25-02

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FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

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U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
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OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/982,835

DATE: 06/25/2002

TIME: 10:06:43

Input Set : A:\gl5047u2.txt

Output Set: N:\CRF3\06252002\I982835.raw

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:
 6 (i) APPLICANT: RABIN, Mark B.
 8 (ii) TITLE OF INVENTION: MUTATIONS IN THE BRCA1 GENE
 10 (iii) NUMBER OF SEQUENCES: 10
 12 (iv) CORRESPONDENCE ADDRESS:
 13 (A) ADDRESSEE: Morgan, Lewis & Bockius LLP
 14 (B) STREET: 1111 Pennsylvania Avenue, N.W.
 15 (C) CITY: Washington
 16 (D) STATE: DC
 17 (E) COUNTRY: USA
 18 (F) ZIP: 20004
 20 (v) COMPUTER READABLE FORM:
 21 (A) MEDIUM TYPE: Diskette
 22 (B) COMPUTER: IBM Compatible
 23 (C) OPERATING SYSTEM: Windows
 24 (D) SOFTWARE: FastSEQ for Windows Version 2.0b
 26 (vi) CURRENT APPLICATION DATA:
 C--> 27 (A) APPLICATION NUMBER: US/09/982,835
 C--> 28 (B) FILING DATE: 17-Jun-2002
 34 (vii) PRIOR APPLICATION DATA:
 31 (A) APPLICATION NUMBER: US 09/038,946
 32 (B) FILING DATE: 1998-03-12
 35 (A) APPLICATION NUMBER: US 09/697,149
 36 (B) FILING DATE: 2000-10-27
 38 (viii) ATTORNEY/AGENT INFORMATION:
 39 (A) NAME: Michael S. Tuscan, Ph.D.
 40 (B) REGISTRATION NUMBER: 43,210
 41 (C) REFERENCE/DOCKET NUMBER: 44921-5047-02-US
 43 (ix) TELECOMMUNICATION INFORMATION:
 44 (A) TELEPHONE: 202-739-3000
 45 (B) TELEFAX: 202-739-3001

ERRORED SEQUENCES

48 (2) INFORMATION FOR SEQ ID NO: 1:
 50 (i) SEQUENCE CHARACTERISTICS:
 51 (A) LENGTH: 5710 base pairs
 52 (B) TYPE: nucleic acid
 53 (C) STRANDEDNESS: single
 54 (D) TOPOLOGY: linear
 57 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Sequence is 5711
in length.

RAW SEQUENCE LISTING

DATE: 06/25/2002

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TIME: 10:06:43

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59	AGCTCGCTGA	GACTTCCTGG	ACCCCGCACC	AGGCTGTGGG	GTTTCTCAGA	TAAGTGGGCC	60
60	CCTGCGCTCA	GGAGGCCTTC	ACCCTCTGCT	CTGGGTAAAG	TTCATTGGAA	CAGAAAGAAA	120
61	TGGATTTATC	TGCTCTTCGC	GTTGAAGAAG	TACAAAATGT	CATTAATGCT	ATGCAGAAAA	180
62	TCTTAGAGTG	TCCCATCTGT	CTGGAGTTGA	TCAAGGAACC	TGTCTCCACA	AAGTGTGACC	240
63	ACATATTTTG	CAAATTTTGC	ATGCTGAAAC	TTATCAACCA	GAAGAAAGGG	CCTTCACAGT	300
64	GTCCTTTATG	TAAGAATGAT	ATAACCAAAA	GGAGCCTACA	AGAAAGTACG	AGATTTAGTC	360
65	AACTTGTTGA	AGAGCTATTG	AAAATCATTT	GTGCTTTTCA	GCTTGACACA	GGTTTGGAGT	420
66	ATGCAACAG	CTATAATTTT	GCAAAAAAGG	AAAATAACTC	TCCTGAACAT	CTAAAAGATG	480
67	AAGTTTCTAT	CATCCAAAGT	ATGGGCTACA	GAAACCGTGC	CAAAAGACTT	CTACAGAGTG	540
68	AACCCGAAAA	TCCTTCCTTG	CAGGAAACCA	GTCTCAGTGT	CCAACCTCTT	AACCTTGGAA	600
69	CTGTGGAAC	TCTGAGGACA	AAGCAGCGGA	TACAACCTCA	AAAGACGTCT	GTCTACATTG	660
70	AATTGGGATC	TGATTTCTCT	GAAGATACCG	TTAATAAGGC	AACTTATTGC	AGTGTGGGAG	720
71	ATCAAGAATT	GTTACAAATC	ACCCCTCAAG	GAACCAGGGA	TGAAATCAGT	TTGGATTCTG	780
72	CAAAAAAGGC	TGCTTGTGAA	TTTTCTGAGA	CGGATGTAAC	AAATACTGAA	CATCATCAAC	840
73	CCAGTAATAA	TGATTTGAAC	ACCACTGAGA	AGCGTGCAGC	TGAGAGGCAT	CCAGAAAAGT	900
74	ATCAGGGTAG	TTCTGTTTCA	AACTTGCATG	TGGAGCCATG	TGGCACAAAT	ACTCATGCCA	960
75	GCTCATTACA	GCATGAGAAC	AGCAGTTTAT	TACTCACTAA	AGACAGAATG	AATGTAGAAA	1020
76	AGGCTGAATT	CTGTAATAAA	AGCAAAACAG	CTGGCTTAGC	AAGGAGCCAA	CATAACAGAT	1080
77	GGGCTGGAAG	TAAGGAAACA	TGTAATGATA	GGCGGACTCC	CAGCACAGAA	AAAAAGGTAG	1140
78	ATCTGAATGC	TGATCCCTTG	TGTGAGAGAA	AAGAATGGAA	TAAGCAGAAA	CTGCCATGCT	1200
79	CAGAGAATCC	TAGAGATACT	GAAGATGTTT	CTTGGATAAC	ACTAAATAGC	AGCATTGAGA	1260
80	AAGTTAATGA	GTGGTTTTTC	AGAAGTGATG	AACTGTTAGG	TTCTGATGAC	TCACATGATG	1320
81	GGGAGTCTGA	ATCAAATGCC	AAAGTAGCTG	ATGTATTGGA	CGTTCTAAAT	GAGGTAGATG	1380
82	AATATTCTGG	TTCTTCAGAG	AAAATAGACT	TACTGGCCAG	TGATCCTCAT	GAGGCTTTAA	1440
83	TATGTAAAAG	TGAAAGAGTT	CACTCCAAAT	CAGTAGAGAG	TAATATTGAA	GACAAAATAT	1500
84	FTGGGAAAAAC	CTATCGGAAG	AAGGCAAGCC	TCCCAACTT	AAGCCATGTA	ACTGAAAATC	1560
85	TAATTATAGG	AGCATTTGTT	ACTGAGCCAC	AGATAATACA	AGAGCGTCCC	CTCACAATA	1620
86	AATTAAAGCG	TAAAAGGAGA	CCTACATCAG	GCCTTCATCC	TGAGGATTTT	ATCAAGAAAG	1680
87	CAGATTTGGC	AGTTCAAAAAG	ACTCCTGAAA	TGATAAATCA	GGGAACCTAAC	CAAACGGAGC	1740
88	AGAATGGTCA	AGTGATGAAT	ATTACTAATA	GTGGTCATGA	GAATAAAACA	AAAGGTGATT	1800
89	CTATTCAGAA	TGAGAAAAAT	CCTAACCCAA	TAGAATCACT	CGAAAAAGAA	TCTGCTTTCA	1860
90	AAACGAAAGC	TGAACCTATA	AGCAGCAGTA	TAAGCAATAT	GGAACCTGAA	TTAAATATCC	1920
91	ACAATTCAAA	AGCACCTAAA	AAGAATAGGC	TGAGGAGGAA	GTCTTCTACC	AGGCATATTC	1980
92	ATGCGCTTGA	ACTAGTAGTC	AGTAGAAATC	TAAGCCCACC	TAATTGTACT	GAATTGCAAA	2040
93	TTGATAGTTG	TTCTAGCAGT	GAAGAGATAA	AGAAAAAATA	GTACAACCAA	ATGCCAGTCA	2100
94	GGCACAGCAG	AAACCTACAA	CTCATGGAAG	GTAAGAAGCC	TGCAACTGGA	GCCAAGAAGA	2160
95	GTAACAAGCC	AAATGAACAG	ACAAGTAAAA	GACATGACAG	TGATACTTTC	CCAGAGCTGA	2220
96	AGTTAACAAA	TGCACCTGGT	TCTTTTACTA	AGTGTTCAAA	TACCAGTGAA	CTTAAAGAAT	2280
97	TTGTCAATCC	TAGCCTTCCA	AGAGAAGAAA	AAGAAGAGAA	ACTAGAAACA	GTTAAAGTGT	2340
98	CTAATAATGC	TGAAGACCCC	AAAGATCTCA	TGTTAAGTGG	AGAAAGGGTT	TTGCAAACTG	2400
99	AAAGATCTGT	AGAGAGTAGC	AGTATTTCAC	TGGTACCTGG	TACTGATTAT	GGCACTCAGG	2460
100	AAAGTATCTC	GTTACTGGAA	GTTAGCACTC	TAGGGAAGGC	AAAAACAGAA	CCAAATAAAT	2520
101	GTGTGAGTCA	GTGTGCAGCA	TTTGAAAACC	CCAAGGGACT	AATTCATGGT	TGTTCCAAAG	2580
102	ATAATAGAAA	TGACACAGAA	GGCTTTAAGT	ATCCATTGGG	ACATGAAGTT	AACCACAGTC	2640
103	GGGAAACAAG	CATAGAAATG	GAAGAAGTGT	AACTTGATGC	TCAGTATTTG	CAGAATACAT	2700
104	TCAAGGTTTC	AAAGCGCCAG	TCATTTGCTC	TGTTTTCAAA	TCCAGGAAAT	GCAGAAGAGG	2760
105	AATGTGCAAC	ATTCTCTGCC	CACCTGGGTT	CCTTAAAGAA	ACAAAGTCCA	AAAGTCACTT	2820
106	TTGAATGTGA	ACAAAAGGAA	GAAAATCAAG	GAAAGAATGA	GTCTAATATC	AAGCCTGTAC	2880
107	AGACAGTTAA	TATCACTGCA	GGCTTTCCTG	TGGTTGGTCA	GAAAGATAAG	CCAGTTGATA	2940

RAW SEQUENCE LISTING

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TIME: 10:06:43

Input Set : A:\gl5047u2.txt

Output Set: N:\CRF3\06252002\I982835.raw

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108 ATGCCAAATG TAGTATCAAA GGAGGCTCTA GGTTTTGTCT ATCATCTCAG TTCAGAGGCA 3000
109 ACGAAACTGG ACTCATTACT CCAAATAAAC ATGGACTTTT ACAAACCCCA TATCGTATAC 3060
110 CACCACTTTT TCCCATCAAG TCATTGTGTA AAATAAATG TAAGAAAAAT CTGCTAGAGG 3120
111 AAAACTTTGA GGAACATTCA ATGTCACCTG AAAGAGAAAT GGGAAATGAG AACATTCCAA 3180
112 GTACAGTGAG CACAATTAGC AATGAATAACA TTAGAGAAAA TGTTTTTAAA GGAGCCAGCT 3240
113 CAAGCAATAT TAATGAAGTA GGTTCAGTA CTAATGAAGT GGGCTCCAGT ATTAATGAAA 3300
114 TAGGTTCCAG TGATGAAAAC ATTCAAGCAG AACTAGGTAG AAACAGAGGG CCAAATTTGA 3360
115 ATGCTATGCT TAGATTAGGG GTTTTGCAAC CTGAGGTCTA TAAACAAAGT CTTCTGGAA 3420
116 GTAATTGTAA GCATCCTGAA ATAAAAAGC AAGAATATGA AGAAGTAGTT CAGACTGTTA 3480
117 ATACAGATTT CTCTCCATAT CTGATTTTCTG ATAACCTAGA ACAGCCTATG GGAAGTAGTC 3540
118 ATGCATCTCA GGTTTGTTCT GAGACCTGT AGACCTGTT AGATGATGGT GAAATAAAGG 3600
119 AAGACTGGA TTTTGCTGAA AATGACATTA AGGAAAGTTC TGCTGTTTTT AGCAAAAGCG 3660
120 TCCAGAGAGG AGAGCTTAGC AGGAGTCTTA GCCCTTTCAC CCATACACAT TTGGCTCAGG 3720
121 GTTACCGAAG AGGGGCCAAG AAATTAGAGT CCTCAGAAGA GAACCTATCT AGTGAGGATG 3780
122 AAGAGCTTCC CTGCTTCCAA CACTTGTTAT TTGGTAAAGT AAACAATATA CTTCTCAGT 3840
123 CTACTAGGCA TAGCACCGTT GCTACCGAGT GTCTGTCTAA GAACACAGAG GAGAATTTAT 3900
124 TATCATTGAA GAATAGCTTA AATGACTGCA GTAACCAGGT AATATTGGCA AAGGCATCTC 3960
125 AGGAACATCA CCTTAGTGAG GAAACAAAAT GTTCTGCTAG CTTGTTTTCT TCACAGTGCA 4020
126 GTGAATTGGA AGACTTGACT GCAAATACAA ACACCCAGGA TCCTTTCTTG ATTGGTTCTT 4080
127 CCAAACAAAT GAGGCATCAG TCTGAAAGCC AGGGAGTTGG TCTGAGTGAC AAGGAATTGG 4140
128 TTTAGATGA TGAAGAAAGA GGAACGGGCT TGCAAGAAAA TAATCAAGAA GAGCAAAGCA 4200
129 TGGATTCAAA CTTAGGTGAA GCAGCATCTG GGTGTGAGAG TGAAACAAGC GTCTCTGAAG 4260
130 ACTGCTCAGG GCTATCCTCT CAGAGTGACA TTTAAACCAC TCAGCAGAGG GATACCATGC 4320
131 AACATAACCT GATAAAGCTC CAGCAGGAAA TGGCTGAAC AGAAGCTGTG TTAGAACAGC 4380
132 ATGGGAGCCA GCCTTCTAAC AGCTACCCTT CCATCATAAG TGAATCCTCT GCCCTTGAGG 4440
133 ACCTGCGAAA TCCAGAACAA AGCACATCAG AAAAAGCAGT ATTAACCTCA CAGAAAAGTA 4500
134 GTGAATACCC TATAAGCCAG AATCCAGAAG GCCTTTCTGC TGACAAGTTT GAGGTGTCTG 4560
135 CAGATAGTTC TACCAGTAAA AATAAAGAAC CAGGAGTGGA AAGGTCATCC CTTCTAAAT 4620
136 GCCCATCATT AGATGATAGG TGGTACATGC ACAGTTGCTC TGGGAGTCTT CAGAATAGAA 4680
137 ACTACCCATC TCAAGAGGAG CTCATTAAAG TTGTTGATGT GGAGGAGCAA CAGCTGGAAG 4740
138 AGTCTGGGCC ACACGATTTG ACGGAAACAT CTACTTGCC AAGGCAAGAT CTAGAGGGAA 4800
139 CCCCTTACCT GGAATCTGGA ATCAGCCTCT TCTCTGATGA CCCTGAATCT GATCCTTCTG 4860
140 AAGACAGAGC CCCAGAGTCA GCTCGTGTG GCAACATACC ATCTTCAACC TCTGCATTGA 4920
141 AAGTTCCCA ATTGAAAGTT GCAGAATCTG CCCAGGGTCC AGCTGCTGCT CATACTACTG 4980
142 ATACTGCTGG GTATAATGCA ATGGAAGAAA GTGTGAGCAG GGAGAAGCCA GAATTGACAG 5040
143 CTTCAACAGA AAGGGTCAAC AAAAGAAATGT CCATGGTGGT GTCTGGCCTG ACCCCAGAAG 5100
144 AATTTATGCT CGTGTACAAG TTTGCCAGAA AACACCACAT CACTTTAACT AATCTAATTA 5160
145 CTGAAGAGAC TACTCATGTT GTTATGAAAA CAGATGCTGA GTTTGTGTGT GAACGGACAC 5220
146 TGAATATATT TCTAGGAATT GCGGGAGGAA AATGGGTAGT TAGCTATTTT TGGGTGACCC 5280
147 AGTCTATTAA AGAAAGAAAA ATGCTGAATG AGCATGATTT TGAAGTCAGA GGAGATGTGG 5340
148 TCAATGGAAG AAACCACCAA GGTCCAAAGC GAGCAAGAGA ATCCCAGGAC AGAAAGATCT 5400
149 TCAGGGGGCT AGAAATCTGT TGCTATGGGC CCTTCACCAA CATGCCACA GATCAACTGG 5460
150 AATGGATGGT ACAGCTGTGT GGTGCTTCTG TGGTGAAGGA GCTTTCATCA TTCACCCTTG 5520
151 GCACAGGTGT CCACCCAATT GTGGTTGTGC AGCCAGATGC CTGGACAGAG GACAATGGCT 5580
152 TCCATGCAAT TGGGCAGATG TGTGAGGCAC CTGTGGTGAC CCGAGAGTGG GTGTTGGACA 5640
153 GTGTAGCACT CTACCAAGTGC CAGGAGCTGG ACACCTACCT GATACCCAG ATCCCCACA 5700
E--> 154 GCCACTACTG A 5710
156 (2) INFORMATION FOR SEQ ID NO: 2:
158 (1) SEQUENCE CHARACTERISTICS:

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sequence is 57110

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159      (A) LENGTH: 1863 amino acids
160      (B) TYPE: amino acid
161      (C) STRANDEDNESS: single
162      (D) TOPOLOGY: linear
164      (ii) MOLECULE TYPE: protein
166      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
168 Met Asp Leu Ser Ala Leu Arg Val Glu Glu Val Gln Asn Val Ile Asn
169   1      5      10      15
170 Ala Met Gln Lys Ile Leu Glu Cys Pro Ile Cys Leu Glu Leu Ile Lys
171      20      25      30
172 Glu Pro Val Ser Thr Lys Cys Asp His Ile Phe Cys Lys Phe Cys Met
173      35      40      45
174 Leu Lys Leu Leu Asn Gln Lys Lys Gly Pro Ser Gln Cys Pro Leu Cys
175      50      55      60
176 Lys Asn Asp Ile Thr Lys Arg Ser Leu Gln Glu Ser Thr Arg Phe Ser
177      65      70      75      80
178 Gln Leu Val Glu Glu Leu Leu Lys Ile Ile Cys Ala Phe Gln Leu Asp
179      85      90      95
180 Thr Gly Leu Glu Tyr Ala Asn Ser Tyr Asn Phe Ala Lys Lys Glu Asn
181      100     105     110
182 Asn Ser Pro Glu His Leu Lys Asp Glu Val Ser Ile Ile Gln Ser Met
183      115     120     125
184 Gly Tyr Arg Asn Arg Ala Lys Arg Leu Leu Gln Ser Glu Pro Glu Asn
185      130     135     140
186 Pro Ser Leu Gln Glu Thr Ser Leu Ser Val Gln Leu Ser Asn Leu Gly
187      145     150     155     160
188 Thr Val Arg Thr Leu Arg Thr Lys Gln Arg Ile Gln Pro Gln Lys Thr
189      165     170     175
190 Ser Val Tyr Ile Glu Leu Gly Ser Asp Ser Ser Glu Asp Thr Val Asn
191      180     185     190
192 Lys Ala Thr Tyr Cys Ser Val Gly Asp Gln Glu Leu Leu Gln Ile Thr
193      195     200     205
194 Pro Gln Gly Thr Arg Asp Glu Ile Ser Leu Asp Ser Ala Lys Lys Ala
195      210     215     220
196 Ala Cys Glu Phe Ser Glu Thr Asp Val Thr Asn Thr Glu His His Gln
197      225     230     235     240
198 Pro Ser Asn Asn Asp Leu Asn Thr Thr Glu Lys Arg Ala Ala Glu Arg
199      245     250     255
200 His Pro Glu Lys Tyr Gln Gly Ser Ser Val Ser Asn Leu His Val Glu
201      260     265     270
202 Pro Cys Gly Thr Asn Thr His Ala Ser Ser Leu Gln His Glu Asn Ser
203      275     280     285
204 Ser Leu Leu Leu Thr Lys Asp Arg Met Asn Val Glu Lys Ala Glu Phe
205      290     295     300
206 Cys Asn Lys Ser Lys Gln Pro Gly Leu Ala Arg Ser Gln His Asn Arg
207      305     310     315     320
208 Trp Ala Gly Ser Lys Glu Thr Cys Asn Asp Arg Arg Thr Pro Ser Thr
209      325     330     335
210 Glu Lys Lys Val Asp Leu Asn Ala Asp Pro Leu Cys Glu Arg Lys Glu

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260 Thr Val Lys Val Ser Asn Asn Ala Glu Asp Pro Lys Asp Leu Met Leu
261                               740                               745                               750
262 Ser Gly Glu Arg Val Leu Gln Thr Glu Arg Ser Val Glu Ser Ser Ser
263                               755                               760                               765
264 Ile Ser Leu Val Pro Gly Thr Asp Tyr Gly Thr Gln Glu Ser Ile Ser
265                               770                               775                               780
266 Leu Leu Glu Val Ser Thr Leu Gly Lys Ala Lys Thr Glu Pro Asn Lys
267                               785                               790                               795                               800
268 Cys Val Ser Gln Cys Ala Ala Phe Glu Asn Pro Lys Gly Leu Ile His
269                               805                               810                               815
270 Gly Cys Ser Lys Asp Asn Arg Asn Asp Thr Glu Gly Phe Lys Tyr Pro
271                               820                               825                               830
272 Leu Gly His Glu Val Asn His Ser Arg Glu Thr Ser Ile Glu Met Glu
273                               835                               840                               845
274 Glu Ser Glu Leu Asp Ala Gln Tyr Leu Gln Asn Thr Phe Lys Val Ser
275                               850                               855                               860
276 Lys Arg Gln Ser Phe Ala Leu Phe Ser Asn Pro Gly Asn Ala Glu Glu
277                               865                               870                               875                               880
278 Glu Cys Ala Thr Phe Ser Ala His Ser Gly Ser Leu Lys Lys Gln Ser
279                               885                               890                               895
280 Pro Lys Val Thr Phe Glu Cys Glu Gln Lys Glu Glu Asn Gln Gly Lys
281                               900                               905                               910
282 Asn Glu Ser Asn Ile Lys Pro Val Gln Thr Val Asn Ile Thr Ala Gly
283                               915                               920                               925
284 Phe Pro Val Val Gly Gln Lys Asp Lys Pro Val Asp Asn Ala Lys Cys
285                               930                               935                               940
286 Ser Ile Lys Gly Gly Ser Arg Phe Cys Leu Ser Ser Gln Phe Arg Gly
287                               945                               950                               955                               960
288 Asn Glu Thr Gly Leu Ile Thr Pro Asn Lys His Gly Leu Leu Gln Asn
289                               965                               970                               975
290 Pro Tyr Arg Ile Pro Pro Leu Phe Pro Ile Lys Ser Phe Val Lys Thr
291                               980                               985                               990
292 Lys Cys Lys Lys Asn Leu Leu Glu Glu Asn Phe Glu Glu His Ser Met
293                               995                               1000                               1005
294 Ser Pro Glu Arg Glu Met Gly Asn Glu Asn Ile Pro Ser Thr Val Ser
295                               1010                               1015                               1020
296 Thr Ile Ser Arg Asn Asn Ile Arg Glu Asn Val Phe Lys Gly Ala Ser
E--> 297 1025                               1030                               1035                               104
298 Ser Ser Asn Ile Asn Glu Val Gly Ser Ser Thr Asn Glu Val Gly Ser
299                               1045                               1050                               1055
300 Ser Ile Asn Glu Ile Gly Ser Ser Asp Glu Asn Ile Gln Ala Glu Leu
301                               1060                               1065                               1070
302 Gly Arg Asn Arg Gly Pro Lys Leu Asn Ala Met Leu Arg Leu Gly Val
303                               1075                               1080                               1085
304 Leu Gln Pro Glu Val Tyr Lys Gln Ser Leu Pro Gly Ser Asn Cys Lys
305                               1090                               1095                               1100
306 His Pro Glu Ile Lys Lys Gln Glu Tyr Glu Glu Val Val Gln Thr Val
E--> 307 1105                               1110                               1115                               112
308 Asn Thr Asp Phe Ser Pro Tyr Leu Ile Ser Asp Asn Leu Glu Gln Pro

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move number
1 space to left or
use less amino
acids per line

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Input Set : A:\gl5047u2.txt

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309          1125          1130          1135
310 Met Gly Ser Ser His Ala Ser Gln Val Cys Ser Glu Thr Pro Asp Asp
311          1140          1145          1150
312 Leu Leu Asp Asp Gly Glu Ile Lys Glu Asp Thr Ser Phe Ala Glu Asn
313          1155          1160          1165
314 Asp Ile Lys Glu Ser Ser Ala Val Phe Ser Lys Ser Val Gln Arg Gly
315          1170          1175          1180
316 Glu Leu Ser Arg Ser Pro Ser Pro Phe Thr His Thr His Leu Ala Gln
E--> 317 1185          1190          1195          120
318 Gly Tyr Arg Arg Gly Ala Lys Lys Leu Glu Ser Ser Glu Glu Asn Leu
319          1205          1210          1215
320 Ser Ser Glu Asp Glu Glu Leu Pro Cys Phe Gln His Leu Leu Phe Gly
321          1220          1225          1230
322 Lys Val Asn Asn Ile Pro Ser Gln Ser Thr Arg His Ser Thr Val Ala
323          1235          1240          1245
324 Thr Glu Cys Leu Ser Lys Asn Thr Glu Glu Asn Leu Leu Ser Leu Lys
325          1250          1255          1260
326 Asn Ser Leu Asn Asp Cys Ser Asn Gln Val Ile Leu Ala Lys Ala Ser
E--> 327 1265          1270          1275          128
328 Gln Glu His His Leu Ser Glu Glu Thr Lys Cys Ser Ala Ser Leu Phe
329          1285          1290          1295
330 Ser Ser Gln Cys Ser Glu Leu Glu Asp Leu Thr Ala Asn Thr Asn Thr
331          1300          1305          1310
332 Gln Asp Pro Phe Leu Ile Gly Ser Ser Lys Gln Met Arg His Gln Ser
333          1315          1320          1325
334 Glu Ser Gln Gly Val Gly Leu Ser Asp Lys Glu Leu Val Ser Asp Asp
335          1330          1335          1340
336 Glu Glu Arg Gly Thr Gly Leu Glu Glu Asn Asn Gln Glu Glu Gln Ser
E--> 337 1345          1350          1355          136
338 Met Asp Ser Asn Leu Gly Glu Ala Ala Ser Gly Cys Glu Ser Glu Thr
339          1365          1370          1375
340 Ser Val Ser Glu Asp Cys Ser Gly Leu Ser Ser Gln Ser Asp Ile Leu
341          1380          1385          1390
342 Thr Thr Gln Gln Arg Asp Thr Met Gln His Asn Leu Ile Lys Leu Gln
343          1395          1400          1405
344 Gln Glu Met Ala Glu Leu Glu Ala Val Leu Glu Gln His Gly Ser Gln
345          1410          1415          1420
346 Pro Ser Asn Ser Tyr Pro Ser Ile Ile Ser Asp Ser Ser Ala Leu Glu
E--> 347 1425          1430          1435          144
348 Asp Leu Arg Asn Pro Glu Gln Ser Thr Ser Glu Lys Ala Val Leu Thr
349          1445          1450          1455
350 Ser Gln Lys Ser Ser Glu Tyr Pro Ile Ser Gln Asn Pro Glu Gly Leu
351          1460          1465          1470
352 Ser Ala Asp Lys Phe Glu Val Ser Ala Asp Ser Ser Thr Ser Lys Asn
353          1475          1480          1485
354 Lys Glu Pro Gly Val Glu Arg Ser Ser Pro Ser Lys Cys Pro Ser Leu
355          1490          1495          1500
356 Asp Asp Arg Trp Tyr Met His Ser Cys Ser Gly Ser Leu Gln Asn Arg
E--> 357 1505          1510          1515          152

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see page 6

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Output Set: N:\CRF3\06252002\I982835.raw

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358 Asn Tyr Pro Ser Gln Glu Glu Leu Ile Lys Val Val Asp Val Glu Glu
359                      1525                      1530                      1535
360 Gln Gln Leu Glu Glu Ser Gly Pro His Asp Leu Thr Glu Thr Ser Tyr
361                      1540                      1545                      1550
362 Leu Pro Arg Gln Asp Leu Glu Gly Thr Pro Tyr Leu Glu Ser Gly Ile
363                      1555                      1560                      1565
364 Ser Leu Phe Ser Asp Asp Pro Glu Ser Asp Pro Ser Glu Asp Arg Ala
365                      1570                      1575                      1580
366 Pro Glu Ser Ala Arg Val Gly Asn Ile Pro Ser Ser Thr Ser Ala Leu
E--> 367 1585                      1590                      1595                      160
368 Lys Val Pro Gln Leu Lys Val Ala Glu Ser Ala Gln Gly Pro Ala Ala
369                      1605                      1610                      1615
370 Ala His Thr Thr Asp Thr Ala Gly Tyr Asn Ala Met Glu Glu Ser Val
371                      1620                      1625                      1630
372 Ser Arg Glu Lys Pro Glu Leu Thr Ala Ser Thr Glu Arg Val Asn Lys
373                      1635                      1640                      1645
374 Arg Met Ser Met Val Val Ser Gly Leu Thr Pro Glu Glu Phe Met Leu
375                      1650                      1655                      1660
376 Val Tyr Lys Phe Ala Arg Lys His His Ile Thr Leu Thr Asn Leu Ile
E--> 377 1665                      1670                      1675                      168
378 Thr Glu Glu Thr Thr His Val Val Met Lys Thr Asp Ala Glu Phe Val
379                      1685                      1690                      1695
380 Cys Glu Arg Thr Leu Lys Tyr Phe Leu Gly Ile Ala Gly Gly Lys Trp
381                      1700                      1705                      1710
382 Val Val Ser Tyr Phe Trp Val Thr Gln Ser Ile Lys Glu Arg Lys Met
383                      1715                      1720                      1725
384 Leu Asn Glu His Asp Phe Glu Val Arg Gly Asp Val Val Asn Gly Arg
385                      1730                      1735                      1740
386 Asn His Gln Gly Pro Lys Arg Ala Arg Glu Ser Gln Asp Arg Lys Ile
E--> 387 1745                      1750                      1755                      176
388 Phe Arg Gly Leu Glu Ile Cys Cys Tyr Gly Pro Phe Thr Asn Met Pro
389                      1765                      1770                      1775
390 Thr Asp Gln Leu Glu Trp Met Val Gln Leu Cys Gly Ala Ser Val Val
391                      1780                      1785                      1790
392 Lys Glu Leu Ser Ser Phe Thr Leu Gly Thr Gly Val His Pro Ile Val
393                      1795                      1800                      1805
394 Val Val Gln Pro Asp Ala Trp Thr Glu Asp Asn Gly Phe His Ala Ile
395                      1810                      1815                      1820
396 Gly Gln Met Cys Glu Ala Pro Val Val Thr Arg Glu Trp Val Leu Asp
E--> 397 1825                      1830                      1835                      184
398 Ser Val Ala Leu Tyr Gln Cys Gln Glu Leu Asp Thr Tyr Leu Ile Pro
399                      1845                      1850                      1855
400 Gln Ile Pro His Ser His Tyr
401                      1860

```

See page 6

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/982,835

DATE: 06/25/2002

TIME: 10:06:44

Input Set : A:\gl5047u2.txt

Output Set: N:\CRF3\06252002\I982835.raw

L:27 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:28 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]

L:154 M:254 E: No. of Bases conflict, Input:5710 Counted:5711 SEQ:1

L:154 M:204 E: No. of Bases differ, LENGTH:Input:5710 Counted:5711 SEQ:1

L:297 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2

M:332 Repeated in SeqNo=2